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cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
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cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
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US-09-867-550-1344
US-09-990-415A-8
US-10-014-338-2
US-10-014-338-4
US-09-990-415A-6
US-09-990-415A-6
US-09-990-415A-6
US-10-094-749-2165
US-10-264-237-2468
US-10-106-698-6940
US-10-106-698-6940
US-09-972-708-9
US-10-104-047-3006
US-10-306-133-3
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Sequence 2, Appli
Sequence 1344, Ap
Sequence 8, Appli
Sequence 2, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 2165, Ap
Sequence 2468, Ap
Sequence 1, Appli
Sequence 6940, Ap
Sequence 9, Appli
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equence 3	Sequence 37	equence 5	equence 5	equence 5	equence 5	equence 5	equence 5	equence 5	equence 5	equence 5	equence 5	equence 5	equence 5	equence 5	equence 5	equence 5	equence 5	equence 5	equence 5	equence 5	equence 6	equence 4	equence 5	equence	equence 6	equence	equence	equence 6	equence
6, Ap	6, App	3, Ap	3, Ap	3, Ap	3, Ap	3, Ap	3, Ap	3, Ap	3, Ap	3, Ap	3, Ap	3, Ap	3, Ap	3, Ap	3, Ap	3, Ap	3, Ap	3, Ap	3, Ap	3, Ap	App1	Appl	3, Ap	3, Ap	Appl	שי	3, Ap	App	Ţ

ALIGNMENTS

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RESULT 1
US-09-990-415A-2
; Sequence 2, Application US/0999041...
; Patent No. US20020165182A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia AB
; TITLE OF INVENTION: Protein Cluster I
; FILE REFERENCE: 00349
; CURRENT APPLICATION NUMBER: US/09/990,415A
; CURRENT FILING DATE: 2001-11-21
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
LENGTH: 261
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Similarity 100.0%; Pred. No. 2.2e-141;
51; Conservative 0; Mismatches 0; Indels 0;
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APPLICANT: Topper, James
TITLE OF INVENTION: No. US20020082206A1el Pc
TITLE OF INVENTION: Thereby
FILE REFERENCE: 21402-013 (Cura-313)
CURRENT APPLICATION NUMBER: US/09/867,550
CURRENT FILING DATE: 2001-09-20
PRIOR APPLICATION NUMBER: USSN 60/208,427
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 2125
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1344
LENGTH: 266
TYPE: PRT
ORGANISM: Homo sapiens
US-09-867-550-1344
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US-09-9
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; Sequence 1344, Application
; Patent No. US20020082206A1
; GENERAL INFORMATION:
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APPLICANT: Pharmacia AB
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Best Local Similarity 100.0%;
Matches 261; Conservative
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APPLICANT:
                                                                                                                TITLE OF INVENTION: Protein Clus
FILE REFERENCE: 00349
CURRENT APPLICATION NUMBER: US/0
CURRENT FILING DATE: 2001-11-21
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.0
TYPE: PRT
ORGANISM: human
FEATURE:
NAME/KEY: misc_f
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Pred. No. 2.2e-141;
; Mismatches 0;
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Publication No. US20030092614A1;
GENERAL INFORMATION:
APPLICANT: Herath, et al.
TITLE OF INVENTION: ADPI-41, A NOVEL PROTEIN
TITLE OF INVENTION: USES THEREFOR
FILE REFERENCE: 9195-077;
CURRENT APPLICATION NUMBER: US/10/014,338
CURRENT FILING DATE: 2002-05-01
PRIOR APPLICATION NUMBER: 10/014,338
PRIOR FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 322
TYPE: PRT
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Best Local Sim
Matches 201;
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|MNTLEKKAFLK 258
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RESULT (
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Publication No. US20030092614A1;
GENERAL INFORMATION:
APPLICANT: Herath, et al.
TITLE OF INVENTION: ADPI-41, A NOVEL PR
TITLE OF INVENTION: USES THEREFOR
FILE REFERENCE: 9195-077;
CURRENT APPLICATION NUMBER: US/10/014,3;
CURRENT FILING DATE: 2002-05-01
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US-10-014-338-4
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Best Local S
Matches 147
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                                                                                                                                                                                                                                                                            Sequence 6, Application US/09990415A
Patent No. US20020165182A1
GENERAL INFORMATION:
APPLICANT: Pharmacia AB
TITLE OF INVENTION: Protein Cluster
FILE REFERENCE: 00349
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Best Local Similarity 79.6%;
Matches 156; Conservative 2
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CURRENT FILING DATE: 2001-11-
NUMBER OF SEQ ID NOS: 8
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PRIOR APPLICATION NUMBER: 10/014,338
PRIOR FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
                                                                                                                                                         TYPE: PRT
ORGANISM: human
09-990-415A-6
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ORGANISM: Homo
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                                                                     NIQEPRWDQSTFLGRARHFFTVTDPRNLLLSGAQLEASRNIVQNYRAGVVTPGITEDQLW
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larity 59.0%;
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Pred.
                                                                                                    Score 753; DB 10;
Pred. No. 3.2e-75;
. Mismatches 65;
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No. 4.5e-89;
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; ORGANISM: Homo
US-10-094-749-2165
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FILE OF INVENTION: NOVEL FULL-LENGTH cDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: Patentin Ver. 2 1
SEQ ID NO 2165
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RESULT 8
US-09-990-415A-4
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WAKAMATSU, AI
SATO, HIROYUKI
ISHII, SHIZUKO
YAMAMOTO, JUN-ICHI
ISONO, YUUKO
HIO, YURI
OTSUKA, KAORU
NAGAI, KEIICHI
IRIE, RYOTARO
TAMECHIKA, ICHIRO
SEKI, NAOHIKO
YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
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OTSUKI, TI
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SFNALVNYTNRNAASPTSVRK 163
                                                                         SFNAIVNYSNRSGDTPITVRQ 149
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Sequence

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ation US/09990415A

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RESULT 9
US-10-264-237-2468
US-10-264-237-2468; Sequence 2468, Application US/10264237; Publication No. US20040009491A1; GENERAL INFORMATION:
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US-10-415-378-1
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                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Nucleic Acids, Proteins, FILE REFERENCE: PA131P1
CURRENT APPLICATION NUMBER: US/10/264,237
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/16450
PRIOR FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: US 60/205,515
PRIOR FILING DATE: 2000-05-19
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TITLE OF INVENTION: Protein C
FILE REFERENCE: 00349
CURRENT APPLICATION NUMBER: U
CURRENT FILING DATE: 2001-11
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.
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Sequence 1, Application US/1041 Publication No. US20040014945A1 GENERAL INFORMATION: APPLICANT: INCYTE CORPORATION;
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NUMBER OF SEQ ID NOS: 2876
SOFTWARE: PatentIn Ver. 3.1
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TYPE: PRT
ORGANISM: human
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10-264-237-2468
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TYPE: PRT
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SANJANWAL
ARVIZU, C
LAL, Pree
KHAN, Far
THORNTON,
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LAL, Preeti G.; AZIMZAI, Yalda;
KHAN, Farrah A.; THANGAVELU, Kavitha;
THORNTON, Michael B.; LU, Dyung Aina M.;
TRIBOULEY, Catherine M.; WARREN, Bridget A.;
ISON, H. Craig; DAS, Debopriya;
RAUMANN, Brigette E.; POLICKY, Jennifer L.;
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II, Ameena R.; DING, Li;
NWALA, Madhusudan M.; RAMKUMAR,
/FTYFFKRTQYFR 278
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NUMBER: US 60/249,661
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NUMBER: US 60/252,232
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NUMBER: PCT/US01/46055
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RESULT 11
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; TITLE OF INVENTION: Colon and Colon Cancer As:
FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: Patentin Ver. 3.0
                                                                                                                                                                                   SEQ ID NO 9
LENGTH: 83
TYPE: PRT
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LOCATION: (14)
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LOCATION: (28)
OTHER INFORMATION: Xaa e
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CURRENT FILING DATE: 2001-
NUMBER OF SEQ ID NOS: 29
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APPLICANT: Wiley, Stev
TITLE OF INVENTION: HEN
FILE REFERENCE: 3160-B
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NAME/KEY: MISC_FEATURE
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Mosley, Bruce A.
Bird, Timothy A.
DuBose, Robert F.
Wiley, Steven R.
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                                                                              IGRMSAQ----VPMNMTITGCMLTF
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LENGTH: 49
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application Publication No. US2003(GENERAL INFORMATION:
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CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 4096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE:
          STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/10/306,133
FILING DATE: 27-No. US20030100485A1-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals,
CTREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                 TITLE
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Similarity 26.7%;
17; Conservative 2
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APPLICATION NUMBER: US/09/009,841
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Pred. No. 0.43;
2; Mismatches
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SEQUENCE CHARACTERISTICS:
LENGTH: 344 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
APPLICANT:
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equence 523, Application
atent No. US20020156006A1
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REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEPAX: 650-845-4166
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SEQUENCE DESCRIPTION:
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52; Conservative 2
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                                                                                           Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
                                                                 Kuo, Sophia S.
Napier, Mar.
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Tumas, Dar
Williams,
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                    Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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Filvaroff, Ellen
Fong, Sherman
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Botstein, David
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TITLE OF INVENTION:
FILE REFERENCE: P26301
CURRENT APPLICATION NI
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TE: 2001-10-15
NUMBER: 09/918585
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NUMBER: 60/
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NUMBER: 60/080194
: 1998-03-31
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: 1998-03-31
NUMBER: 60/080107
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: 1998-03-27
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NUMBER: 60/079663
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: 1998-03-27
NUMBER: 60/079689
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1998-03-26
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NUMBER: 60/078910
: 1998-03-20
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NUMBER: 60/077649
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NUMBER: 60/077632
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AC ABP6
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PN 27-1
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                                                                                         Cytostatic; Cardiant; Anti-allergic; Immunosuppressive; Vulnerary; Antiinflammatory; gene therapy; human; ORFX; atherogenic; platelet human umbilical vein endothelial cell; HUVEC; atherosclerotic plaque cancer; cardiovascular disease; allergy; autoimmune disease; wound healing; blood coagulation disorder; inflammatory disorder.
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N-PSDB;
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site at seqdata.uspto.gov/sequence.html?DocID=20020082206.
                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 10;
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(MEHR/)
(CONL/)
(TOPP/)
(LAWD/)
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                                             VFWQWVNQSFNAIVNYSNRSGDTPITVRQLGTAYVSATTGAVATALGLKSLTKHLPPLVG
               IPAMAIPPLIMDTLEKKDFLK 261
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65.
                                                                                           VNQSFNAIVNYSNRSGDTPITVRQLGTAYVSATTGAVATALGLKSLTKHLPPLVG
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PPLIMDTLEKKDFLK 261
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CC ABL39691 to ABL39818 represent novel human nucleic acid sequences encoding the proteins given in ABB06037 to ABB06164. The novel sequences (NS) can have cytostatic, osteopathic, gynaecological, neuroprotective, antirheumatic, antiarthritic, antipsoriatic, ophthalmological, virucide, vasotropic, antiarteriosclerotic, antiinflammatory, dermatological, cardiovascular, anticoagulant, antifibrinolytic, hypotension, antiasthmatic, cardiant, cardicer, antidepressant, gastrointestinal, aeuroleptic, tranquilliser, antiulcer, antidepressant, gastrointestinal, aeuroleptic, cerebroprotective, nootropic and contraceptive activities. The NS can be used in vaccines, gene therapy and antisense therapy. Nucleic acids, expression vectors and ciagnosing e.g. cancer, osteoporosis, endometriosis, degenerative diseases, dystonia, multiple sclerosis, rheumatoid arthritis, psoriasis, cataracts, restenosis, atherosclerosis, inflammation, skin disorders, glaucoma, obesity, muscular dystrophy, AIDS, infertility, cardiovascular disease, epilepsy, angina, neurodegeneration, diabetes, anxiety, depression, schizophrenia, viral disease, gastric ulcers, stroke, CAlzheimer's disease and as a contracentive.
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W antirheumatic; antiarthritic; antipsoriatic; ophthalmological; anti-HIV;
W vasotropic; antiarteriosclerotic; antiinflammatory; dermatological;
W vasotropic; muscular; antiinfertility; cardiovascular; anticoagulant;
W antifibrinolytic; hypotension; antiasthmatic; immunomodulator; cardiant;
W anticonvulsant; antidiabetic; tranquilliser; antidepressant; aeuroleptic;
W gastrointestinal; virucide; antiulcer; cerebroprotective; nootropic;
W contraceptive; vaccine; gene therapy; cancer; osteoporosis; dystonia;
W endometriosis; degenerative disease; multiple sclerosis; psoriasis;
W rheumatoid arthritis; cataract; restenosis; atherosclerosis; glaucoma;
W inflammation; skin disorder; obesity; muscular dystrophy; AIDS;
W inflammation; skin disorder; obesity; muscular dystrophy; hypertension;
W ischaemia; asthma; immune disease; coagulation disease; hypertension;
W diabetes; anxiety; depression; schizophrenia; viral disease; stroke;
W gastric ulcer; Alzheimer's disease.
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glaucoma, ol
disease, coa
disease, epi
depression,
Alzheimer's
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larity 100.0%;
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AC AAM93760;
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FPI 05-SEP-20
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Sequence
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Matches 261; Conservative 0;
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11-JAN-2000;
02-MAY-2000;
                                                                                             The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a polypeptide encoded by a full length human cDNA of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ota T, Ni
Wakamatsu
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DB; AAK94713.
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K, Kojima S, Otsuki
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09-JUL-2000;
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29-NOV-2000;
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Zhao
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and
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N-PSDB; AAI59123.
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                                                                                                                                   17-JUN-1999;
10-AUG-1999;
18-AUG-1999;
28-OCT-1999;
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                 WPI; 2001-0414
N-PSDB; AAF277
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DE Huma
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                                                                                                   Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
W vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
W anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
W immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
W hypotensive; dermatological; immunosuppressive; antidiabetic;
W antiviral; antibacterial; antifungal; antirheumatic; antidiabetic;
W antianaemic; gene therapy; cancer; proliferative disorder; hypertension;
W neurodegenerative disorder; osteoarthritis; graft vs host disease;
W cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
W cholesterol ester storage; systemic lupus erythematosus; infection;
W severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
W allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
W bone damage; cartilage damage; antiinflammatory disease; coagulation;
W thrombosis; contraceptive.
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Matches 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention provides the protein and coding sequences for 43 novel human transport proteins (designated TPPTs). These can be used in the diagnosis and treatment of transport, metabolic, neurological, reproductive, cardiovascular and immune disorders, and cell proliferative disorders such as cancer.
                                                                                                                                                                                                                                                                                     08-FEB-2001
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Similarity 100.0%;
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3.7e-144;
es 0;
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AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, C which represent the human ORFX open reading frames 1 to 3161. The ORFX C sequences have activities such as: cytostatic; hepatotropic; vulnerary; C antipsoriatic; antiparkinsonian; nootropic; neuroprotective; C antipsoriatic; antiparkinsonian; nootropic; neuroprotective; C antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; immunosuppressive; C antidiabetic; hypotensive; dermatological; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating C pathological conditions associated with an ORFX-associated disorder. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, C proliferative disorders, neurodegenerative disorders, osteoarthritis, C profiferation, hypothyroidism, cholesterol ester storage, systemic lupus carterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, coagulation; to inhibit thrombosis; and as a contraceptive.
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Matches
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05-APR-1999;
30-MAR-2000;
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N-PSDB; AAC7579
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Pred. No. 9.2e-136;
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Protein; 397 AA.

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating conciders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations or responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and camino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp. wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 251
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23-AUG-2000;
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
                                                                                                                       The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, such as lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tang
Wang
Zhao
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                                                                                                                                                                  The present invention relates to methods and compositions for the screening, diagnosis or prognosis of Alzheimer's disease (AD) in a subject. The method comprises analysing a sample of brain tissue from a subject by 2D electrophoresis to generate a 2D array of Alzheimer's disease-associated features (ADFs), whose relative abundance correlates with the presence, absence, stage or severity of AD and comparing the abundance of each feature with the abundance of invention also describes Alzheimer's disease-associated protein compositions of the invention are useful for the screening, diagnosis or prognosis of AD in a subject, for determining the stage or severity of AD in a subject, for identifying a subject at risk of developing AD, or for monitoring the effect of therapy administered to a subject thaving AD. Antibodies capable of binding to ADPIs are useful for treatment regime. An agent that modulates the activity of ADPI is useful in the manufacture of a medicament for the treatment or prevention of AD in a subject. The present sequence represents human appert that modulates the activity of ADPI is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Screening, diagnosis or prognosis of Alzheimer's disease in comprises detecting Alzheimer's disease-associated features Alzheimer's disease-associated protein isoforms in brain tis from the subject -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-508575
N-PSDB; ABK96715
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Similarity 78.5%;
01; Conservative
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                                                                                               Score 1089; DB 23
Pred. No. 4.4e-115
; Mismatches 27
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AC ALTERNAY-20;
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                                                                         The present invention relates to the identification of a human gene family (see ABN83754-57) encoding a group of polypeptides (see ABB76445-48) referred to as Protein Cluster I. This family of homologous proteins was identified by an 'all-versus-all' BLAST procedure using all Caenorhabditis elegans proteins in the Compared to the Drosophila melanogaster Plybase database, and mon-annotated protein clusters, conserved in both C. elegans and D. melanogaster, were used in a BLAST procedure against the Celera Human Genome Database, and Protein Cluster I proteins of unknown Cluster I comprises polypeptides encoded by 3 genes. The gene encoding the present polypeptide is expressed primarily in the identification of the tissue(s) or cell type(s) present in a biological sample, for diagnosis of diseases and disorders, especially cobesity and diabetes, and for identifying agents useful in the treatment of such disorders and immune disorders, especially
                                                        identification c
biological sampl
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Query Match

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23;

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RESULT 13
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ID AAE13276
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KW diabetes
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12-APR-2000;
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                                 Polypeptides of diagnosing, transportation neurological,
                                                                                                                                               Reddy R, T
Gandhi AR,
Policky JL,
Walsh RT, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; transporter and ion channel; TRICH; akinesia; cystic fibrosis diabetes mellitus; Parkinson's disease; myasthenia gravis; dementia; cardiac disorder; angina; hypertension; myocarditis; hyperglycaemia; neurological disorder; Alzheimer's disease; cataract; infertility; Wilson's disease; schizophrenia; Grave's disease; addison's disease; Huntington's disease; multiple sclerosis; meningitis; hypotensive; cardiant; nootropic; neuroprotective; neuroleptic; ophthalmological; antithyroid; anticonvulsant; goitre; antiinflammatory.
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Walia NK,
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The invention relates to human transporters and ion channels (TRICH)
and the polynucleotides encoding them. The composition comprising TRICH
or agonist of TRICH is useful for treating a disease or condition
composition associated with decreased expression of functional TRICH or condition
comprising Ab is useful for diagnosing a condition of disease associated
with expression of TRICH in a subject, where the disorders include a
transport disorder such as akinesia, cystic fibrosis, diabetes mellitus,
Parkinson's disease, myasthenia gravis, cardiac disorders associated
with transport e.g. angina, hypertension, myocarditis, neurological
disorders associated with transport e.g. Alzheimer's disease, Wilson's
disease, schizophrenia, cataracts, infertility, hyperglycaemia, Grave's
disease, goitre, addison's disease, Huntington's disease, dementia,
multiple sclerosis, bacterial and viral meningitis. TRICH DNA is useful
for generating a transcript image of a tissue or cell type, which
represents the global pattern of gene expression by a particular tissue
or cell type and for analysing the proteome of a tissue or cell type.
TRICH DNA is used in gene therapy. The present amino acid sequence is
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DNA is
TRICH3
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S Query Matc Best Local Matches 2 Sequence Match σ Simi GELPLD 322 Con lar <u>Α</u> 81.0%; Score 1089; DB 23; ity 78.5%; Pred. No. 4.4e-115; servative 28; Mismatches 27; Length 322; Indels 0 -: Gaps

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멂 Ş 8 183 186 123 AAVAAAN AAVAAA NCINIPLMRQRELQVGIPVADEAGQRLGYSVTAAKQGIFQVVISRICMAIPAMA 242 245

S 밁 243 IPPLIM IPPFIMNTLEKKAFLK 258 DTLEKKOFLK 261

AAB41 85 standa rd; Protein; 332 AA.

AAB41585

FEB-2001 ffi irst entry)

ORF1 349 polypeptide sequence SEQ ID NO:2698.

Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid; antidabeterial; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cholesterol ester storage; osteoarthritis; graft vs host disease; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation; thrombosis; contraceptive.

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                                                                                                                                                                                                                                                                                                         AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antipsoriatic; anticonvulsant; nootropic; newroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressant; cantidiabetic; hypotensive; dermatological; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, coagulation; to inhibit thrombosis; and as a contraceptive.
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30-MAR-2000;
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25-APR-2000;
09-JUL-2000;
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03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
                                                  The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, such as Alzheimer's, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, and thrombolytic activity, chemotactic/chemokinetic activity, haemostatic assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                Novel such a
                                                                                                                                                                                                                                                                                               Tang
Wang
Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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N-PSDB; AAI61354.
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2000US-0662191.

2000US-0693036.

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                                                                                                                                                                                                                               acids and polypeptides, useful nervous system injuries -
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US-08-627-173-20
US-08-535-882A-20
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US-09-252-991A-110S-08-463-620-11
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731 of human granulocyte colony-stimulating
factor-receptor."
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4 73.5 5.5 456 3	equence 1	
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6 73.5 5.5 487 1 US-08-030-644-2	equence 2	
8 73.5 5.5 487 1 US-08-072-063-	equence	
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CORRESPONDENCE ADDRESS: ADDRESSEE: Hoffmann-La Roche Inc. STREET: 340 Kingsland Street		
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TYPE: Floppy ER: PC compat		
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APPLICATION NUME FILING DATE: 31		
PPLICATION NUMBER: US		
FILING DATE: 19-JUL-1993 ATTORNEY/AGENT INFORMATION:		
NAME: Kass, Alan P REGISTRATION NUMBER: 32142		
REFERENCE/DOCKET NUMBER: C		
NE: (201) 235-4		
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SEQUENCE CHARACTERISTICS: LENGTH: 602 amino acids		
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TITLE OF INVENTION: DNA S
STIMULATING FACTOR RECEPTORS
NUMBER OF SEQUENCES: 6
CURRENT APPLICATION DATA:
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Best Local S
Matches 54
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Sequence 4, Application Patent No. 5574136 GENERAL INFORMATION:
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Best Local
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APPLICATION NUMBER: 587,329
FILING DATE: 24-SEP-1990
APPLICATION NUMBER: 522,952
FILING DATE: 03-APR-1990
APPLICATION NUMBER: 416,306
FILING DATE: 03-OCT-1989
APPLICATION NUMBER: 412,816
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APPLICANT: SMITH,
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FILING DATE: 15-JAN-1993
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Similarity 24.9%;
54; Conservative 3
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larity 24.9%;
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26-SEP-1989
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                             US/07923976
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; Pred. No. 0.04
34; Mismatches
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Pred. No. 0.028;
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APPLICATION NUMBER: US/07/923,976 FILING DATE: 19920922 CLASSIFICATION: 435 PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 74539/1990 FILING DATE: 23-MAR-1990 PRIOR APPLICATION NUMBER: JP 176629/1990 FILING DATE: 03-JUL-1990 PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP91/00375 FILING DATE: 22-MAR-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
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07-923-976-4
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TELEFAX: 703-415-1508
INFORMATION FOR SEQ ID NO: 4
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CORRESPONDENCE
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APPLICANT: Fukunaga, Rikiro
TITLE OF INVENTION: DNA Encoding Granulocyte
TITLE OF INVENTION: Colony-Stimulating Factor Receptor
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MEDIUM TYPE: Floppy disk
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Arlington
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Similarity 24.9%; Pred. No. 0.048;
54; Conservative 34; Mismatches
                                                                                                                                                                                                                                                                                                          YRKTPTVVFW-QWVNQSFNAIVNYSNRS----GDTPIT---VRQLGTAYVSATTGAVATA 165
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  PTIMEEDAFQ--
                                                                       -TAAKQGIFQVVISRICMAIPAMAIPPLIMDTLEKKD 258
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Jones, Tullar & Cooper,
). Box 2266 Eads Station
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NUMBER: 51
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RESULT 4
US-07-923-976-8
; Sequence 8, Application US/07923976
; Patent No. 5574136
; GENERAL INFORMATION:
APPLICANT: Nagata, Shigekazu
APPLICANT: Fukunaga, Rikiro

INVENT

Nagata, Shigekazu Fukunaga, Rikiro FENTION: DNA Encoc

DNA Encoding Granulocyte

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Patent No. 63805.

Patent No. 63805.

GENERAL INFORMATION:

APPLICANT: Lynn Douce

TTTT.E OF INVENTION: ]
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Best Local S
Matches 55
                                          Sequence 5531, Application US/09134001C Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/923,976
FILING DATE: 19920922
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 74539/1990
FILING DATE: 23-MAR-1990
PRIOR APPLICATION NUMBER: JP 176629/1990
PRIOR APPLICATION NUMBER: JP 176629/1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP91/00375
FILING DATE: 22-MAR-1991
ATTORNEY/AGENT INFORMATION:
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TELEPHONE: 703-415-1500
TELEFAX: 703-415-1508
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
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COMPUTER:
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CITY: 1
STATE:
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REGISTRATION NUMBER: 28
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE
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Similarity 22.4%;
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IBM PC compatible

SYSTEM: PC-DOS/MS-DOS

Patentin Release #1.0,
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Station
         AND :
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Mismatches
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RESULT 6
US-09-252-991A-18502
; Sequence 18502, Appl
Patent No. 6551795
                                                                                                                                                                ; ORGANISM: Pseudor US-09-252-991A-18502
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                                                                                                                                                              SEQ ID NO 18502
LENGTH: 394
TYPE: PRT
ORGANISM: Pseud
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PRIOR FILING DATE:
NUMBER OF SEQ ID NO
SEQ ID NO 5531
LENGTH: 655
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REFERENCE: GTO
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OR APPLICATION I
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FNPELES
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llarity 20.9%;
Conservative 32
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107196.136
ION NUMBER: US/09/252,991A
ATE: 1999-02-18
N NUMBER: US 60/074,788
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TC-007
ON NUMBER: US/09/134,001C
TE: 1998-08-13
NUMBER: US 60/064,964
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1998-02-18
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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Pred. No. 0.21;
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--TALVVARBWERGTMEAVLS--
                                                    -QFWRAG--LDVAAPAQAVMLEPRYW 189
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US-08-627-17
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STATE: VIKUSA.
STATE: VIKUSA.
COUNTRY: U.S.A.
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
THER: IBM PC compatible
THER: PC-DOS/MS-DOS
THER: TOTAL TYPE
THER: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                              ATTORNEY/ACLIVATION NUMBER: 32,205
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1331
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: 703) 816-4000
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                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 01
FILING DATE: 28-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
FILING DATE: 03-APR-
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
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28-SEP-1995
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Pred. No. 0.13
9; Mismatches
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US-08-535-882A-20
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US-08-316-424A-6
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                                                               Sequence 6, Application; Patent No. 6022848; GENERAL INFORMATION: KOZLOV,
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Patent No
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1331
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEPAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
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                                                  APPLICANT:
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-535-882A-20
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ATTORNEY/AGENT IN
NAME: BYRNE, T
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         TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND TITLE OF INVENTION: USES THEREOF NUMBER OF SEQUENCES: 11
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CORRESPONDENCE
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OPERATING SYS
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                                                                                          6, Application US/08316424A
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                                               KOZLOV, VI
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WOLPE, STEPHEN D.
RENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
RENTION: USES THEREOF
RQUENCES: 27
RCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IBM PC compatible
YSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
CATION DATA:
NUMBER: US/08/535,882A
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ADDRESS:
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                                                            VLADIMIR
                                                    IRBNA
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Pred. No. 0.13;
19; Mismatches 57; Indels
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US-09-005-546-20
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                                                                                                                                                                                                            Patent No. 6090782
GENERAL INFORMATION:
APPLICANT: TSYRLOVA,
APPLICANT: WOLPE, STI
TITLE OF INVENTION: I
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
ADDRESSEE: NIXON &
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/316,424A
FILING DATE: 30-SEP-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1331-122
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4100
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vo
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/no/-
FILING DATE:
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ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STREET: 11
CITY: ARLI
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N: INHIBITOR OF
N: USES THEREOF
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25.8%;
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                                      US/09/005,546
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Pred. No.
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                                                                 Version
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US-08-477-669-6
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US-09-005-546-20
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Patent No. 6432917
GENERAL INFORMATION:
APPLICANT: KOZLOV, VLADIMIR
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Best Local
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                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,669
FILING DATE: 07-Jun-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/316,424
FILING DATE: 30-SEP-1994
ATTORNEY/AGENT INFORMATION:
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TORNEY/AGENT INFORMATION:
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ZIP: 222
COMPUTER REAL
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CORRESPONDEN
                            TELECOMMUNIC
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           NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 13
COMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
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SPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
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larity 25.8%;
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TYPE: Flonny
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2201-4714
                                                                                                                                                                                                                     TYPE: Floppy disk
R: IBM PC compatible
NG SYSTEM: PC-DOS/MS-DOS
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(703)
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INHIBITOR OF STEM CELL PROLIFERATION AND
USES THEREOF
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Pred. No. 0.13;
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                                           1331-122
                                                                                                                                                                                                       Version
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Best Local :
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                                                                                                                                    APPLICATION NUMBER: US/07/923,976
FILING DATE: 19920922
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 74539/1990
FILING DATE: 23-MAR-1990
PRIOR APPLICATION NUMBER: JP 176629/1990
PRIOR APPLICATION NUMBER: JP 176629/1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP91/00375
FILING DATE: 22-MAR-1991
FILING DATE: 22-MAR-1991
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 771 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           atent No.
                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy COMPUTER: IBM PC com
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                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                             ATTORNEY/AGENT INFORMATION:
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STATE: Virg
TTD: 22202
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STREET: P.
                                                                                     NAME: Hellwege, Jam
REGISTRATION NUMBER:
REFERENCE/DOCKET NUM
                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS
                                          TELEFAX:
                                                          TELEPHONE:
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SEQUENCE
7-669-6
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32; Conser
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Fukunaga, Rikii.
Fukunaga, Rikii.
FumTion: DNA Encoding Grain.
FumTion: Colony-Stimulating
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llarity 25.8%;
Conservative
                                          703-415-1500
703-415-1508
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SEQ ID NO 25845
LENGTH: 514
TYPE; PRT
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APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
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APPLICANT: Dijkhuizen, Lubbert
APPLICANT: Dijkhuizen, Bauke
APPLICANT: Andersen, Carsten
APPLICANT: Andersen, Claus von der
TITLE OF INVENTION: Cyclomaltodextrin Glucanotransferase
TITLE OF INVENTION: Variants
FILE REFERENCE: 4285.204-US
CURRENT APPLICATION NUMBER: US/08/947,965A
CURRENT FILING DATE: 1997-10-09
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o. 6551795
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Similarity 29.1%; Pred. No. 1.9;
1; Conservative 21; Mismatches 57; Indels
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NOS: 33142
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RESULT 15
US-09-252-991A-19749
; Sequence 19749, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
RAPPLICANT: MARC J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO 1
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19749
; LENGTH: 621

TYPE: DET
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; EARLIER FILING DATE: 1995-04-21
; EARLIER APPLICATION NUMBER: 1173/95
; EARLIER FILING DATE: 1995-10-17
; EARLIER APPLICATION NUMBER: 1281/95
; EARLIER APPLICATION NUMBER: PCT/DK96/00179
; EARLIER APPLICATION NUMBER: PCT/DK96/00179
; EARLIER FILING DATE: 1996-04-22
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 71
; LENGTH: 676
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-08-947-965-71
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Similarity 21.9%;
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186 AAVAAANCINIPLMRQRELQVGIPVADEAGQRLGYSVTAAKQG	66 ITEDQLWRAKYVYDSAFHPDTGEKVVLIGRMSAQVPMNMTITGC : :: : :	ry Match 79.1%; Score 1064; DB 2; t Local Similarity 77.3%; Pred. No. 1.2e-85; ches 198; Conservative 27; Mismatches 31; 6 GELPLDINIQEPRWDQSTFLGRARHFFTVTDPRNLLLSGA : : : : : : : : 38 GEVPPNINIKEPRWDQSTFIGRASHFFTVTDPKNILLTNE	ALIGNMENTS 10 10 arboxylate carrier - rat (fragment) ecies: Rattus sp. (rat) te: 26-Jul-1996 #sequence_revision 26-Jul-1996 #t cession: I55210 zi, A.; Glerum, M.; Koller, R.; Mertens, W.; Spyc ioenerg. Biomembr. 25, 515-524, 1993 tle: The mitochondrial tricarboxylate carrier. ference number: I55210; MUID:94179133; PMID:81324 cession: I55210 atus: preliminary; translated from GB/EMBL/DDBJ lecule type: mRNA sidues: 1-357 <res> oss-references: GB:S70011; NID:g545997; PIDN:AAB3 perfamily: Saccharomyces probable membrane protei</res>	30 82.5 6.1 519 2 S31136 31 82.5 6.1 625 2 G96976 32 82 6.1 147 1 HBMS 33 82 6.1 382 2 AF0168 34 82 6.1 771 2 B38252 36 82 6.1 1077 2 B38252 37 81.5 6.1 531 2 A55788 38 81.5 6.1 939 2 T18974 39 81.5 6.1 1626 2 A75613 40 81 6.0 324 2 F70609 41 81 6.0 328 2 AE0491 42 81 6.0 914 1 JN0550 44 81 6.0 2505 1 XYRTFA 45 80.5 6.0 356 2 AG0370
KQGIFQVVISRICMAIPAMA 245 	MTITGCMLTFYRKTPTVVFWQW 125 : : : : :	Indels 0; Gaps 0; QLEASRNIVQNYRAGVVTPG 65 : :	ext_change 26-May-2000 her, s. 91 91 0258.1; PID:g545998	nitrogen fixation probable periplasm hemoglobin beta ma probable membrane granulocyte colony gene 26 protein - acriflavin resista glucuronosyltransf hypothetical prote hypothetical prote hypothetical prote probable exported cyclomaltodextrin iodide peroxidase enoyl-[acyl-carrie probable ABC-trans

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RESULT 3
T19996
hypothetical protein C47D12.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #;
C;Accession: T19996
R;Gajadsty, S.
submitted to the EMBL Data Library, March 1996
A;Reference number: Z19209
A;Accession: T19996
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-326 <WIL>
A;Cross-references: EMBL: Z69902; PIDN:CAA93764.1; GS:A;Experimental source: clone C47D12
C;Genetics:
A;Gene: CESP:C47D12.3
A;Map position: 2
A;Introns: 26/1; 116/2; 205/2
C;Superfamily: Saccharomyces probable membrane prote:
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A;Molecule type: DNA
A;Residues: 1-324 <WIL>
A;Cross-references: EMBL:Z66565
A;Experimental source: clone TO
C;Genetics:
A;Gene: CESP:T04F8.1
A;Map position: X
A;Introns: 29/3; 58/2; 172/3; 2
C;Superfamily: Saccharomyces pr
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                       WOWVNOSFNAIVNYSNRSGDTPITVRQLGTAYVSATTGAVATALGLKSLT-
                                                   DPNMTVDELWKAKTLYD
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FHWVNQSFNAIVNYTNRSGTHKQDDRTLILSYCGATTGALSCALSFNYMLKKWKNAPPIL
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probable
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                                                                                                                                                           Score; Pred.
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                                                   DTGEKMFILGRMSAQVPCNMLITGGMLTFYQKLPHVIF
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e membrane
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ed. No. 3.6e-53;
Mismatches 73;
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RESULT 4
T18612
hypothetical protein AH6.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C;Accession: T18612
R;Berks, M.
submitted to the EMBL Data Library, January 1995
A;Reference number: Z18998
A;Accession: T18612
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-329 <WIL>
A;Cross-references: EMBL:Z48009; PIDN:CAA88076.1; GSPDB:GN00020; CESP:AH6.2
A;Experimental source: clone AH6
C;Genetics:
A;Reference number: Z19488
A;Accession: T21924
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-326 <WIL>A;Residues: 1-326 <WIL>A;Cross-references: EMBL:Z81534; PIDN:CAB04347.1; GSPDB:GN00020; CESP:F37H8.4
A;Experimental source: clone F37H8
C;Genetics:
A;Gene: CESP:F37H8.4
A;Map position. 7
                                                                                                                                                                      hypothetical protein F37H8.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change
C;Accession: T21924
R;Gregory, J.
submitted to the EMBL Data Library, November 1996
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A;Map position: 2
A;Introns: 26/1; 99/3; 173/3; 202/2; 245/1
C;Superfamily: Saccharomyces probable membrane protein YOR271c
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RESULT 6
T27337
hypothetical protein Y6E2A.9 - Caenorhabd
C; Species: Caenorhabditis elegans
C; Date: 15-Oct-1999 #sequence_revision 15
C; Accession: T27337
R; Matthews, L.
submitted to the EMBL Data Library, Janua
A; Reference number: Z20347
A; Accession: T27337
A; Status: preliminary; translated from GB
A; Molecule type: DNA
A; Residues: 1-329 <WILL>
A; Cross-references: EMBL: AL021175; PIDN: C
A; Experimental source: clone Y6E2A
C; Genetics:
A; Gene: CESP: Y6E2A.9
A; Map position: 5
A; Introns: 26/1; 99/3; 202/2; 245/1
C; Superfamily: Saccharomyces probable mem
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1 Similarity 47.3%;
121; Conservative 4
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46.6%;
tive 39
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                                                                                                                                                                                                                                                               39,
                                                                                                                                                                                                                                                            Score 593; DB 2; 1
Pred. No. 2.2e-44;
; Mismatches 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 604; DB 2; 1
Pred. No. 2.3e-45;
7; Mismatches 86;
                                                                                                    YFCATGAATTAALGLNMMVKNSHGLAGRLVP
                                                                                                                                                                                                                                                                                                                                                                                               PIDN: CAA15970.1;
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A;Accession: S67168
A;Molecule type: DNA
A;Residues: 1-327 <JAU>
A;Cross-references: EMBL:Z75179; NID:g1420607; PID:g1420608; MIPS:YOR271c
A;Experimental source: S67169
A;Reference number: S67169
A;Reference number: DNA
A;Residues: 1-327 <CHE>
A;Cross-references: EMBL:Z75179; NID:g1420607; PID:g1420608; MIPS:YOR271c
A;Experimental source: strain S288C
R;Cheret, G.; Bernardi, A.; Sor, F.
Yeast 12, 1059-1064, 1996
A;Reference number: S72039; MUID:97051594; PMID:8896271
A;Reference number: S72039; MUID:97051594; PMID:8896271
                                                                                                                                                                                                                                                                                                                                                                                                                                    probable membrane probable membrane probable membrane hype N; Alternate names: hype C; Species: Saccharomyce C; Date: 12-Jul-1996 #8 S
A;Accession:
A;Status: nuc
A;Molecule ty
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T15498
hypothetical protein C14F5.4 - Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #t(C; Accession: T15498 R; Minx, P. submitted to the EMBL Data Library, June 1995
                                                                                                                                                                                                                                                                                                                                                              R;Jauniaux, J.C.; Poirey, R. submitted to the Protein Sequence Database, July 1996 A;Reference number: S67143 A;Accession: S67168
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R; Jauniaux, J.
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A;Introns: 31/3; 82/;
C;Superfamily: hypotl
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A; Residues: 1-285 < M.
A; Cross-references: 1
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A;Accession: T15498
A;Status: preliminary; translated from GB/EMBL/DDBJ
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le type: DNA
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sequence of C. elegans cosmid
: Z18361
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hetical protein C14F5.4
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e: strain Bristol N2
                   id sequence
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                    not shown;
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                    translation not
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                                                                              Saccharomyces
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A;Residues: 1-327 <CHW>
A;Cross-references: EMBL:X89633; NID:g12
A;Note: the nucleotide sequence was subm C;Genetics:
A;Cross-references: SGD:S0005797
A;Map position: 15R
A;Note: YOR271c
C;Superfamily: Saccharomyces probable mate C;Keywords: transmembrane protein F;184-200/Domain: transmembrane #status F;276-292/Domain: transmembrane #status
                                                                                                                                                                                                 RESULT 9
T19873
hypothetical protein C41C4.2 - Caenorhabd
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15
C;Accession: T19873
R;Burton, J.
submitted to the EMBL Data Library, Febru
A;Reference number: Z19190
A;Accession: T19873
A;Status: preliminary; translated from GB
A;Molecule type: DNA
A;Residues: 1-616 <WIL>
A;Cross-references: EMBL:Z48045; PIDN:CAA
A;Experimental source: clone C41C4
C;Genetics:
A;Gene: CESP:C41C4.2
A;Map position: 2
A;Introns: 24/2; 72/3; 214/3; 291/2; 371/
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                                                                                                                                                   100; Conservative 32.28;
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                                                 KLKSAILHPDTG
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NYANRNATOPOPLSKYIGAYGAAVTAACSISGGLTYFIKKASSLPPTTRIIIORFVPLPA
                       NYSNRSGDTPITVRQLGTAYVSATTGAVATALGLKSLTK-
                                                                  YVYDSAFHPDTGEKVVLIGRMSAQVPMN-MTITGCMLTFYRKTPTVVFWQWVNQSFNAIV
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                                                                                                   FLGRYLHCLD
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                                               Caenorhabditis
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                       --LVGRFVPFAA
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probable transporter - fission yeast (Schizosaccharomy, C; Species: Schizosaccharomyces pombe
C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #te:
C; Accession: T37847
R; Murphy, L.; Harris, D.; Barrell, B.G.; Rajandream, M submitted to the EMBL Data Library, September 1997
A; Reference number: Z21749
A; A; Ccession: T37847
A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA
A; Residues: 1-325 < MUR>
A; Cross-references: EMBL:Z99162; PIDN:CAB16226.1; GSPD: A; Experimental source: strain 972h-; cosmid c17G6
C; Genetics:
                                                      A; Reference number: A81
A; Accession: E81461
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-326 < PYL:
A; Cross-references: GB
A; Experimental C; Genetics: A; Gene: MTCC
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T02841
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                                                                                                                                                      R;Myler, P.J.; Audleman, L.; deVos, T.; Hixson, G.; Kiser, P.; Lemley, C.; Magness, C.; Proc. Natl. Acad. Sci. U.S.A. 96, 2902-2906, 1999
A;Title: Leishmania major Friedlin chromosome 1 has an unusual distribution of protein-A;Reference number: A81455; MUID:99178987; PMID:10077609
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A;Map position: 1
A;Introns: 33/2; 70/1; 94/3; 206/3
C;Superfamily: Saccharomyces probable membrane protein YOR271c
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C;Date: 24-Mar-1999
C;Accession: E81461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, he EMBL Data Library, September 1997
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ccharomyces pombe
#sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
                                      GB:AE001274; NID:g3264850; PIDN:AAC24664.1;
ce: strain MHOM/IL/81/Friedlin
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RESULT 12
A99514
hypothetical protein MYPU_0170 [imported] - Mycoplasma pulmonis (st C; Species: Mycoplasma pulmonis
C; Species: Mycoplasma pulmonis
C; Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-C; Accession: A99514
R; Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Gali Nucleic Acids Res. 29, 2145-2153, 2001
A; Title: The complete genome sequence of the murine respiratory pat A; Reference number: A99512; MUID:21267165; PMID:11353084
A; Accession: A99514
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-791 <KUR>
A; Cross-references: GB:AL445566; PID:g14089430; PIDN:CAC13190.1; GS
A; Experimental source: strain UAB CTIP
C; Genetics:
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C; Superfamily: S
C; Keywords: mitc
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A;Genetic code: SGC3
C;Superfamily: phosphotransferase
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59; Conservative
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Similarity 30.9%;
30; Conservative
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45; Mis
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C;Species: Homo sapiens (man)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #
C;Accession: JH0329; S21608
R;Larsen, A.; Davis, T.; Curtis, B.M.; Gimpel, S.; S
J. Exp. Med. 172, 1559-1570, 1990
A;Title: Expression cloning of a human granulocyte of a human granulating facenta a high a source: placenta of a human granulating facenta figure of a human granulating facenta fi
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T40295

fructosyl amine - fission ye
fructosyl amine - fission ye
C; Species: Schizosaccharomyc
C; Date: 03-Dec-1999 #sequenc
C; Accession: T40295
R; Wood, V.; Rajandream, M.A.
submitted to the EMBL Data L
A; Reference number: Z21918
A; Accession: T40295
A; Status: preliminary; trans
A; Molecule type: DNA
A; Residues: 1-412 <WOO>
A; Cross-references: EMBL:ALO
A; Experimental source: strai
C; Genetics:
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larity 20.6%;
Conservative 3
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B:X55720; NID:g31698; PIDN:CAA39252.1; PID:g31699
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Data Library, March 1998
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Pred. No. 1.5;
7; Mismatches
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Mismatches 93; Indels
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RESULT 15

I56551

neurotrimin - rat?
C;Species: Rattus:norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 19-May-2000
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 19-May-2000
C;Accession: I56551
R;Struyk, A.F.; Canoll, P.D.; Wolfgang, M.J.; Rosen, C.L.; D'Eustachio, P.; Salzer, J.L.
J. Neurosci. 15, 2141-2156, 1995
A;Title: Cloning of neurotrimin defines a new subfamily of differentially expressed neur
A;Reference number: I56551; MUID:95198094; PMID:7891157
A;Accession: I56551
A;Accession: I56551
A;Roseule type: mRNA
A;Residues: 1-344 <RES>
A;Cross-references: EMBL:U16845; NID:g755184; PIDN:AAA67445.1; PID:g755185
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
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Similarity 24.8%; Pred. No. 3.4;
52; Conservative 28; Mismatches
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Pfam; PF03820; Mtc; 1.

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Sideroflexin
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STRAIN=Sprague-Dawley;
Mashima H., Kojima I.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases
-!- FUNCTION: Potential iron transporter.
-!- SUBCELLULAR LOCATION: Mitochondrial (By similarity)
-!- SIMILARITY: Belongs to the sideroflexin family.
-!- SIMILARITY: Belongs to the sideroflexin family.
   EMBL; }
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                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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RECUENCE FROM N.A. (ISOFORM 2).

RP SEQUENCE FROM N.A. (ISOFORM 2).

RA SEQUENCE FROM N.A. (ISOFORM 2).

RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,

RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Schonbach C., Gojobori T.,

RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Nikaido I., Osato N., Saito R., Nogami A., Schonbach C., Gojobori T.,

RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,

RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

Balla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,

RA Gassterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

RA Gassterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,

Detrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
                                                                                                                                                                                                        Eukaryota; Metazu., C Mammalia; Eutheria; Rodentia, ...

X NCBI_TaxID=10090;

RN [1]

RN SEQUENCE FROM N.A. (ISOFORM 1), AND TISSUE SPECIFICITY.

RN SEQUENCE FROM N.A. (ISOFORM 1), AND TISSUE SPECIFICITY.

RN MEDLINE=21172735; PubMed=11274051;

RA Andrews N.C.;

RA Andrews N.C.;

RT "A mutation in a mitochondrial transmembrane protein is responsible for the pleiotropic hematological and skeletal phenotype of flexed-tail (f/f) mice.";

Genes Dev. 15:652-657(2001).
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Best Local &
Matches 245
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Q91V61; Q8C1Z2;
28-FEB-2003 (Rel
28-FEB-2003 (Rel
15-SEP-2003 (Rel
Sideroflexin 3.
SFXN3.
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TIGRFAMS; T
Transport;
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SEQUENCE
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nalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
__TaxID=10090;
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s; TIGR00798; mt
rt; Iron transpo
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174
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245 Pi
286 Pi
35433 MW;
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sport; Iron; Mitochondrion; Transmembrane
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Last sequence update)
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61D9DE679A7E6124 CRC64;
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RA Sultana R., Takenaka Y., Taylor M.S., Teaddale R.D., Tomita M., Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C., Wang Y., Watanabe Y., Walls C., Rogers J., Wang Y., Watanabe Y., Sakazume N., Sakazu
                                                                                           EMBL; AF325262; AAK39430.1;
EMBL; AK089985; BAC41029.1;
EMBL; BC012208; AAH12208.1;
MGD; MGI:2137679; Sfxn3.
InterPro; IPR004686; Mtc.
Pfam; PF03820; Mtc; 1.
ProDom; PD006986; Mtc; 1.
TIGRFAMS; TIGR00798; mtc; 1.
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Sandelin A
Sultana R.
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                                                                   Transport;
Alternative
                                                                                                                                                                                                                                                                                                                                                                    Note=No experimental confirmation TISSUE SPECIFICITY: Widely expressed SIMILARITY: Belongs to the siderofle
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IsoId=Q91V61-2;
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1700 to 1746 1746 1746 225 2266
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194
245
286
                                                                                 ransport;
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Y., Taylor M.S.,
Wahlestedt C., 1
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POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
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sideroflexin
                                                                                    Mitochondrion;
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                                                                                                                                                                                                                                                                                                                                                                                                                           available;
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                                                                                 Transmembrane;
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RESULT 4
SFX1_HUMD
ID SFX1
AC Q9HS
DT 28-I
DT 28-I
DT 15-I
DT 15-I
OC FUK
OC Mam
OC NCB
RN [1]
RR FR SEQ
RA ISC
RA Van
RA Wat
RA Wat
RA Wat
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RA A1
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Best Lo
Matcher
SEQUENCE OF 19-3;
TISSUE=Lung;
TISSUE=Lung;
MEDLINE=22388257,
Strausherg R.L.,
Klausner R.D., Co
Altschul S.F., Zo
Hopkins R.F., Jo
Diatchenko L., Ma
Stapleton M., Soa
Brownstein M.J.,
Raha S.S., Loquel
Bosak S.A., McEwa
Richards S., Worl
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                                                                                                                                                                                               TISSUB-Mammary gland, and Teratocarcinoma;
Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
Ninomiya K., Iwayanagi T.;
"NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                              [2]
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HUMAN STANDARD; PRT; 322 AA.
SPX1 HUMAN STANDARD; PRT; 322 AA.
Q9H9B4; Q9HA53;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Sideroflexin 1.
SFXN1.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARSPLIC
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R.L., Feingold E.A., Grouse L.H., Derge J.G.,
D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              243
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rity 95.3%;
nservative
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the EMBL/GenBank/DDBJ database
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9B9816A54B23F4BC
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RESULT 5
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A Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
A Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
Droc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
C-!- FUNCTION: Might be involved in the transport of a component
required for iron utilization into or out of the mitochondria.
C-!- SUBCELLULAR LOCATION: Mitochondrial (By similarity).
C-!- SUBCELLULAR LOCATION: Mitochondrial (By similarity).
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Best Local Similarity
Matches 201; Conser
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EMBL; AK022287; BAB14003.1; A
EMBL; AK0222938; BAB14318.1; A
EMBL; BC020517; AAH20517.1; A
Genew; HGNC:16085; SFXN1.
InterPro; IPR004686; Mtc.
Pfam; PF03820; Mtc; 1.
ProDom; PD006986; Mtc; 1.
TIGRFAM8; TIGR00798; mtc; 1.
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MSGELPPNINIKEPRWDQSTFIGRANHFFTVTDPRNILLTN
EQLESARKIVHDYRQGIVPPGL -> MI (IN REF. 2;
BAB14003).

Y -> K (IN REF. 2; BAB14318).

Y -> K (IN REF. 2; BAB14318).

SSMSVTSLEAELQAKIQESHPELRRVYFNKGL -> RYVFV
IRQNHHEY (IN REF. 2; BAB14003).

MW; 47E03172F27990DB CRC64;
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ALT_INIT.
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Pfam; PF03820; Mtc; 1.
ProDom; PD006986; Mtc; 1.
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J. Bioenerg. Biom
-!- FUNCTION: Mig!
required for:
-!- SUBCELLULAR LG
-!- TISSUE SPECIF:
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Sideroflexin
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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TISSUE=Liver;
MEDLINE=94179133; PubMed=8132491;
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MEDLINE=22388257; PubMed=12477932;

X MEDLINE=2388257; PubMed=12477932;

X MEDLINE=2388257; PubMed=12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

A Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Golbs R.A.,

Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

A Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

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Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Bochnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences.",

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

-I FINSUE SPECIFICITY: Widely expressed, with highest expression in

C. -I TISSUE SPECIFICITY: Widely expressed, with highest 
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Sideroflexin
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Genes Dev. 15:652-657(2001).
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STRAIN=C57BL/6J; TISSUE=Embryo;
STRAINE=21085660; PubMed=11217851;
MEDLINE=21085660; PubMed=11217851;
Kawai J., Shinagawa A., Shibata K.,
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Hayashizaki Y.;
"Functional annota
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MOUSE SFX2 MOUSE Q925N2; Q925N2; 28-FEB-2003 (28-FEB-2003 (15-SEP-2003 (Sideroflexin SFXN2.

(Rel (Rel (Rel 2.

> 441, 22,

Created)
Last sequence update)
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RESULT SFX2_M

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PRT;

322 AA.

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MBL; AK012650; -

MBL; BC005743; A

%D; MGI:2137677;

%GO:0005739; C

%GO:0005739; C

%GO:0006826; P:

%erPro; IPR00468

m; PF03820; Mtc

Dom; PD006986; 1

RFAM8; TIGR00798

18PORT; Iron tra

ISMEM 103

SMEM 147

SMEM 175

SMEM 175

SMEM 267

%MEM 267

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%MEM 267

%MEM 322 AA;
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DISEASE: Defects in SFXN1 are the cause of a transitory hypochromic, microcytic anemia characterized by a large number of siderocytes containing non-heme iron granules. The anemia begins at 12 dpc, is most intense at 15 dpc and is still severe at birth, but disappears by 2 weeks of age. Mutant adults are no longer anemic, but they have an impaired response to hemopoietic stress. Most homozygotes also have flexed tails and a belly spot. SIMILARITY: Belongs to the sideroflexin family.

CAUTION: REF. 2 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
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                                        TLEKKAPLK 258
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C:mitochondrion; IDA.
P:erythrocyte differentiation;
P:iron ion transport; IMP.
                     TLEKKOFLK 261
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77.3%; Pred. No. 2e-8
ive 26; Mismatches
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X MEDLINE=22388257; PubMed=12477932;
A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.
A Klausner R.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Diatchenko L., Warusina K., Farmer A.A., Rubin G.M., Hong L.,
A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.
A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Blakesley R.W., Touchman J.W., Green E.J., Lu X., Gibbs R.A.,
A Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
A Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
A Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
A Butterfield Sci. U.S.A. 99:16899-16903 (2002).

T "Generation and initial analysis of more than 15,000 full-length
T human and mouse cDNA sequences.",
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

- I- FUNCTION: Potential iron transporter.
- I- SUBCELLULAR LOCATION: Mitochondrial (By similarity).
- I- TISSUE SPECIFICITY: Expressed in brain, heart, kidney, spleen
                                                Query Ma
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Matches
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NCBI_TaxID=10090;
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L; BC019808; AAH19808.1;
; MGI:2137678; Sfxn2.
erPro; IPR004686; Mtc.
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SIMILARITY: Belongs to the sideroflexin
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om; PD006986; Mtc;
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Q96NB2;
28-FEB-2003 (
28-FEB-2003 (
15-SEP-2003 (
Sideroflexin
                     "NEDO human cDNA Submitted (OCT-2 -! FUNCTION: Po -! SUBCELLULAR -! SIMILARITY:
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Mammalia; Eutheria; Primates;
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, Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,
Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A.,
., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,
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(Rel. 41, Last sequence update)
(Rel. 42, Last annotation update)
2.
                   DNA sequencing project.";
T-2001) to the EMBL/GenBank/DDBJ databases
Potential iron transporter.
AR LOCATION: Mitochondrial (By similarity)
Y: Belongs to the sideroflexin family.
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Genew; HGNC:16086; SFXN2.
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ProDom; PD006986; Mtc; 1.
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YP22 CAEEL STANDARD; PRT
Q09201;
01-NOV-1995 (Rel. 32, Created)
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15-SEP-2003 (Rel. 42, Last annotated)
Hypothetical protein AH6.2 in chromatory
AH6.2.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromabditidae; Peloderinae; Caenorhance Rhabditidae; Peloderinae; Caenorhance SEQUENCE FROM N.A.
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44; Mismatches 83
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P SEQUENCE FROM N.A. (ISOFORM 2).

P MEDLINE=22354683; PubMed=12466851;

X MEDLINE=22354683; PubMed=12466851;

X Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,

A Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa Y.,

A Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa Y.,

A Najari K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobor A.,

Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

Baldarelli R., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,

A Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,

Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousin A.

Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousin A.,

Blake J.A., Bradt D., Brusic V., Chothia C., Godzik A., Gough J.,

Gastimond T., Gariboldi M., Gissi C., Godzik A., Gough J.,

A Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.I.

Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

A Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

A Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole
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Q925N0; Q8BGG3;
28-FEB-2003 (Rel. 4
15-SEP-2003 (Rel. 4
15-SEP-2003 (Rel. 4
sideroflexin 5.
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Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
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InterPro;
Pfam; PF03
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***Pro; IPR004686; Mtc.
**; PF03820; Mtc; 1.
**)om; PD006986; Mtc; 1.
**FAMs; TIGR00798; mtc; 1
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RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K., RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C., RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L., Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K., RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yahayashiraki Y., Barney E., Hayashizaki Y., Birney E., Hayashizaki Y., Birney E., Hayashizaki Y., Ishi Y., Lander E.S., Rogers J., Birney E., Hayashizaki Y., Ishi Y., Ishi Y., Ishi Y., Ishi Y., Ishi Y., Birney E., Hayashizaki Y., Materston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y., Ishi 
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"A mutation in a mitochondrial transmembrane protein is responsible for the pleiotropic hematological and skeletal phenotype of flexed-tail (f/f) mice.";

Genes Dev. 15:652-657(2001).

-!- FUNCTION: Potential iron transporter.

-!- SUBCELLULAR LOCATION: Mitochondrial (By similarity).

-!- TISSUE SPECIFICITY: Expressed in liver and brain.

-!- SIMILARITY: Belongs to the sideroflexin family.
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MEDLINE=21172735; PubMed=11274051;
Fleming M.D., Campagna D.R., Haslett J.N., Trenor C.C.
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ity 38.3%; Pred. No. 1.5e-35;
servative 50; Mismatches 99;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Durbin R.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential)
-!- SIMILARITY: BELONGS TO THE C.ELEGANS RECEPTOR-LIKE PROTEIN
                                                                                                                        y Match
Local Similarity 40.0%;
hes 100; Conservative
                                          103
                                                              76
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ŃŶAŃŔNATQPQPLSKYIGAYGAAVTAACSISGGLTYFIKKASSLPPTTRIIIQŔFVPLPA
                                                                                                   EPRWDQSTFLGRARHFFTVTDPRNLLLSGAQLEASRNIVQNYRAGVVTPGITEDQLWRAK
                   NYSNRSGDTPITVROLGTAYVSATTGAVATALGLKSLTK--
                                                           YVYDSAFHPDTGEKVVLIGRMSAQVPMN-MTITGCMLTFYRKTPTVVFWQWVNQSFNAIV
                                          KLKSAILH
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                                                                                  JGRYLHCLDVIDPRTLFASNKKLE
                                        EKVLPPFRMSGFVPFGWITVTG
                                                                                                                        Score 432.5; DB 1;
Pred. No. 1.2e-30;
43; Mismatches 96;
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Sideroflexin
SFXN4.
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the Euro
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Eukaryota; Metazoa; Chordata;
Mammalía; Eutheria; Rodentia;
NCBI_TaxID=10090;
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for the pleiotropic
flexed-tail (f/f) mi
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MGD; MGI:2137680;
InterPro; IPR0046
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND TISSUE SPECIFICITY. MEDLINE=21172735; PubMed=11274051; Fleming M.D., Campagna D.R., Haslett J.N., Andrews N.C.;
                                                                                                                                                                                                                                                                        ProDom;
                                                                                                                                                                                                                                                                                     Pfam;
                                                                                                                                                                                                                                                                                                                      ween the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way lifted and this statement is not removed. Usage by and for commercial ties requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
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PF03820; Mtc; 1.
m; PD006986; Mtc; 1.
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KSIILT(
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                                                                     QLWRAK
                     PTVVFWQWVNQSFNAIVNYSNRSGD---TPITVRQLGT-AYVSAT-TGAVATALGLKSLT
                                                                                          MEPNLQFWISERQAFFRRFCQWMDLLDPVNMFISIGSIEKSRQLLFT--
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ity 20.7%;
servative 50
                                                                                                                                                                                                                                                transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a mitochondrial transmembrane protein is responsible opic hematological and skeletal phenotype of f) mice."; 52-657(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
SCLYGYTTAFNITNGNASYSHGÞVERTLLGAGVFVSSTFIGLIPHLFQMKY---

    41, Created)
    41, Last sequence up
    41, Last annotation

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                                              IYLDNQVIKDAWNKSLSTVHÞDSSKLIPHLFRÞAAFLÞVTAÞMVFLLMMÞDTGI 107
                                                                     45.
                                                                                                                                                                                                                                                                                                                                                                                                                                      tential iron transporter.
LOCATION: Mitochondrial (By similarity).
[FICITY: Largely restricted to kidney, brain and heart
Belongs to the sideroflexin family.
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191
247
289
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Pred: No. 0.011;
50; Mismatches 1
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POTENTIAL.
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                                                                   SAFHPDTGEKVVLIGRMSAQVPMNMTITGCMLTFYRKT 117
                                                                                                                                                                                       ACF650B711A7552F CRC64;
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                                                                                                                                                              DB 1;
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[4]

SEQUENCE F.

P SEQUENCE F.

P SEQUENCE F.

P GLN-440; HIS->.

RA Rieder M.J., Arme.

RA Rajkumar N., Toth E.J.

RL Submitted (SEP-2002) to L.

RL Submitted (SEP-2002) to L.

RN [5]

RP DOMAINS STRUCTURE.

MEDLINE=92007729; PubMed=1717255;

Fukunaga R., Ishizaka-Ikeda E., Proceeding of the granule                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ş
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[3]
SEQUENCE FROM N.A.
MEDLINE=92091782; PubMed=1530796
Seto Y., Fukunaga R., Nagata S.;
"Chromosomal gene organization ostimulating factor receptor.";
T Immunol. 148:259-266(1992).
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GCSR_HUMAN
GCSR_HUMAN
GCSR_HUMAN

O99062;

01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
Granulocyte colony stimulating factor recepto:
(CD114 antigen).
CSF3R OR GCSFR.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertel
Mammalia; Eutheria; Primates; Catarrhini; Hom.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
TISSUE=Placenta;
MEDLINE=91079757; PubMed=2147944;
Larsen A., Davis T., Curtis B.M., Gimpel S., i
Park L., Sorensen E., March C.J., Smith C.A.;
"Expression cloning of a human granulocyte col
receptor: a structural mosaic of hematopoietii
immunoglobulin, and fibronectin domains.";
J. Exp. Med. 172:1559-1570(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [2]
SEQUENCE FROM N.A.
TISSUE=Placenta;
MEDLINE=91062348; Pu
Fukunaga R., Seto Y.
"Three different mRN
factor receptor.";
factor natl. Acad. So
 Dong F., Hoefsloot I
Veerman A.J., Touw I
"Identification of a
stimulating factor I
Proc. Natl. Acad. So
[7]
STRUCTURE BY NMR OF
MEDLINE=97331327; Po
Yamasaki K., Naito S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          229
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.J., Armel T.Z., Carrington D.P., Ozu. N., Toth E.J., Yi Q., Nickerson D.A. i (SEP-2002) to the EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; PubMed=1701053
co Y., Mizushima
c mRNAs encoding
l OF 227-334.
1; PubMed=918765
Lto S., Anaguchi
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                                                                       pubMed=7514305;

t L.H., Schelen A.M., 1

w I.P., Lowenberg B.;

of a nonsense mutation :

or receptor in severe consci. U.S.A. 91:4480-4
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a E., Pan C.-
granulocyte
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ng human granulocyte o
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congenital neutropenia.";
-4484(1994).
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"Solution structure of an extracell motif of the granulocyte colony-sti interaction with ligand."; Nat. Struct. Biol. 4:498-503(1997). [8]
3D-STRUCTURE MODELING OF 125-331.
MEDLINE=98037802; PubMed=9368043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CSF). IN ADDITION IT MAY FUNCTION IN SOME ADHESION OR RECOGNITION
EVENTS AT THE CELL SURFACE.

IS SUBCULIT: DIMER (PROBABLE).

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. THE GCSFR-2 FORM,
WHICH LACKS THE TRANSMEMBRANE DOMAIN, MAY REPRESENT A SOLUBLE FORM,
OF THE RECEPTOR.

ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=4;
Comment=Additional isoforms seem to exist. Experimental
confirmation may be lacking for some isoforms;
Name=1; Synonyms=GCSFR-1;
IsoId=Q99062-1; Sequence=Displayed;
Name=2; Synonyms=GCSFR-2;
IsoId=Q99062-2; Sequence=VSP_001674;
Name=3; Synonyms=GCSFR-3;
IsoId=Q99062-3; Sequence=VSP_001671, VSP_001672;
Name=4; Synonyms=GCSFR-4, D7;
IsoId=Q99062-4; Sequence=VSP_001671, VSP_001672;
Name=3; SPECIFICITY: ONE OR SEVERAL FORMS HAVE BEEN FOUND IN
MYELOGENOUS LEUKEMIA CELL LINE KG-1, LEUKEMIA U937 CELL LINE, IN
BONE MARROW CELLS, PLACENTA, AND PERIPHERAL BLOOD GRANULOCYTES.
THE GCSFR-2 FORM HAS BEEN FOUND ONLY IN LEUKEMIA U937 CELLS. THE
GSCFR-3 FORM IS HIGHLY EXPRESSED IN PLACENTA.

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J. Biol. Chem. 272:29735-29741(1997).
-!- FUNCTION: RECEPTOR FOR GRANULOCYTE COLONY-STIMULATING FACTOR (G-CSF). IN ADDITION IT MAY FUNCTION IN SOME ADHESION OR RECOGNITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #een the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial ties requires a license agreement (See http://www.isb-sib.ch/announce/
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JR InterPro; IPR003961,
JR InterPro; IPR003529; He...
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L; X55720; CAA39252.1; -.

L; S71484; AAB20660.1; -.

L; M59818; AAA63176.1; -.

BL; M59819; AAA63177.1; -.

BL; M59820; AAA63177.1; -.

BL; M59820; AAA63177.1; -.

BL; M59820; AAA63177.1; -.

R; B38252; B38252.

R; C38252; C38252.

R; JH0329; JH0329.

DB; 1AZ7; 28-JAN-98.

enew; HGNC:2439; CSF3R.

IM; 138971; -.

O; GO:0005887; C:integral to plasma meno; GO:0004872; F:receptor activity; TASC; GO:0006952; P:defense response; TASC; C:integral to plasma membrane; F:receptor activity; TAS. P:defense response; TAS. HEMATOPO_REC_L_F2;

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N-FTId=VSP 001671.

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N-SELPGPROGUMLHPAPPUGLLCLFPITSVL (in isoform 4).

N-STIG=VSP 001673.

EGSELHILLLTCLCGTAMLCCSPNRKNPLWPSV PDPAHSSLGSWVPTIMEEDAFQLPGLGTPPITKLTVLEEDE KKPVPWESHNSSETCGLPTLVQTYVLQGDPRAVSTQPQSQS GTSDQVLYGQLLGSPTSPGGHYLRCDSTQPLLAFILQGIR VHGMEALGSF -> APTGRIPSGQVSQTQLTAAWAPGCPQS WRRMPSSCPALARHPSPSSQCWRRMKRSRCPGSPITAQRPV ASPLWSRPMCSRGTQEQFPPSPNPSLAPAIRSFMGSCWAAP QAQGQGTISAVTPLSPSWRASPPAPSPMRTSGSRPAPWGPW (in isoform 2).

N-TId=VSP 001674.

M-PTIG=VSP 001674.
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EXTRACELLULAR (POTENTIAL)

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

IG-LIKE C2-TYPE.

FIBRONECTIN TYPE-III 1.

FIBRONECTIN TYPE-III 2.

FIBRONECTIN TYPE-III 3.

FIBRONECTIN TYPE-III 4.

FIBRONECTIN TYPE-III 4.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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A Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,

A Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,

A Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,

A Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,

A Nasuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,

A Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;

"NEDO human cDNA sequencing project.";

Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AK074707; BAC11151.1; -.

IR EMBL; AK074707; BAC11151.1; -.

IR InterPro; IPR004686; Mtc.

IR Pfam; PF03820; Mtc; 1.

RYPOTHER TIGRO0798; mtc; 1.

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MEDLINE=22354683; PubMed=12466851;

The FANTOM Consortium,

the RIKEN Genome Exploration Research (
"Analysis of the mouse transcriptome b;
60,770 full-length cDNAs.";

Nature 420:563-573(2002).

EMBL; AK089985; BAC41029.1; -.

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RA Amanatides P.G., Scherer S.E., Li P.M., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
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RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Ballew R.M., Basu A., Baxendale J., Belson C.R., Maklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Berkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
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RA Durbin K.J., Brownes M., Dugan-Rocha S., Dunkov B.C., Chandra I.,
RA Houth K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Hostin D., Houston K., Howland T.J., Wei M.-H., Houck J.,
RA Hostin D., Houston K., Morris J., Houck J.,
RA Hostin D., Houston K., Almand T.J., Wei M.-H., Houck J.,
RA Hostin D., Houston K., Nixon K., Nussern D., McIndon K.A.,
RA McFullov G., Milishina N.V., Mobarry C., Worris J., Moshredi A.,
RA Mount S.M., Mordia C.D., Fran S., Pollard J., Puri v., Reese M.G.,
RA Markellov G., Milishina N.V., Mobarry D.M., Nelson D.L.,
RA Pales R.A., Words T., Stapleton M., Strong R., Sun E.,
RA Spier E., S
Miranda A., Mungall C.J
Patel S., Phouanenavong
Celniker S.;
Submitted (NOV-2002) to
EMBL; AE003606; AAF5213
EMBL; BT001832; AAU7158
FlyBase; FBgn0037239; CV
InterPro; IPR004686; Mto
Pfam; PF03820; Mtc; 1.
TIGRFAMs; TIGR00798; mto
SEQUENCE 321 AA; 357.
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Ephydroidea; Dro
NCBI_TaxID=7227;
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SEQUENCE FROM N.
STRAIN=BERKELEY;
MEDLINE=20196006
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SEQUENCE FR
STRAIN=y;
Stapleton M
Champe M.,
George R.,
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a; Drosophilidae; Drosophila.
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(MAR-2002) to the EMBL/GenBank/DDBJ databases
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14686; Mtc.
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AAN71587.1; -.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence upon the control of the
                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genome sequence of the nematinvestigating biology."; Science 282:2012-2018(1998). EMBL; Z66565; CAA91477.1; -. WormPep; T04F8.1; CE03614. InterPro; IPR004686; Mtc. Pfam; PF03820; Mtc; 1. TIGRFAMS; TIGR00798; mtc; 1. SEQUENCE 324 AA; 35488 MW;
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Science 282:2012-2018(1998).
EMBL; 269902; CAA93764.1; -.
WormPep; C47D12.3; CE05431.
InterPro; IPR004686; Mtc.
Pfam; PF03820; Mtc; 1.
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SEQUENCE 326 AA; 36436 MW;
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C47D12.3 protein.
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Caenorhabditis elegans.
Q9VVW3;
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ty 53.7%; Pred. No. 4.6e-55;
ervative 40; Mismatches 73; Indels
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GPVILEQLSK 259
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X MAN K.H., Doyle C., Baxter E.G., Melt G., Nelson C.R., Miklos G.L.G., May M. M., Claser P., Batchan M. R., Bouck J., Bhandari D., Bolshakov S., Baxter B.G., Change M. P., Bolshakov S., May M. M., Claser P., Borthier P., Downes M., Dugan-Rocha S., Pleischmann W. Borthier P., Gorrell J.H., Gu Z., Guan P., Harris M., Glasser X., Pleischmann W. Melson K.A., Howland T.J., Wei M.-H., Glasser X., Borthier N.J., Melson D.L., Melson D.L., Melson D.L., Melson D.L., Melson D.R., Nelson D.L., Melson D.R., Nelson D.L., Melson D.R., Nelson D.L., Melson D.R., Melson D.R., Melson D.R., Melson D.R., Melson D.R., Melson 
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                                                                   Hradecky P., Huang Y., Kamini
Tupy J.L., Bergman C., Berman
Clamp M., Drysdale R., Emmert
Kronmiller B., Marshall B., N
Searle S.M.J., Smith E., Shu
Ashburner M., Gelbart
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NCBI_TaxID=7
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u S., Smutniak
B B.B., L., Prochn...
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EMBL; AE003518;
FlyBase; FBgn003
InterPro; IPR004
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SEQUENCE 327 A
                                                                 Champe M., Chave, George R., Gonza, Miranda A., Mung, Patel S., Phouan, Celniker S., Submitted (DEC-2), Submitted (DEC-2), EMBL; AY071029; FlyBase; FBgn003, Interpro; IPR003, Interpro; IPR003, Interpro; IPR004, IPR
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SEQUENCE FR
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zoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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46; Mismatches 78;
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Science 282:2012-2018(1)
EMBL; Z81534; CAB04347.;
WormPep; F37H8.4; CE283(
InterPro; IPR004686; Mto
Pfam; PF03820; Mtc; 1.
TIGRFAMS; TIGR00798; mto
SEQUENCE 349 AA; 3935
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F37H8.4 protein.
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Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
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Mismatches 86;
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STRAIN=Bristol N2
MEDLINE=99069613;
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C14F5.4.
Caenorhabditi
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Submitted
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"The
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Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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STRAIN-Bristol N2;
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tted (JUN-1995) to the EMBL/GenBank/DDBJ databases
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(TrEMBLrel. 21, Last sequence update)
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35.3 kDa protein.
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Matches 93
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=22035372; PubMed=12039050;
Lockhart P.J., Holtom B., Lincoln S., Huss Gasser T., Wszolek Z.K., Hardy J., Farrer "The human sideroflexin 5 (SFXN5) gene: stand exclusion as a candidate for PARK3."; Gene 285:229-237(2002).

EMBL; AY044437; AAK95826.1; -.
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Hypothetical )
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Eukaryota; Metazoa; (
Mammalia; Eutheria; I
NCBI_TaxID=9606;
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Science 282:2012-2018(1998)
EMBL; AL021175; CAA15970.2;
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Eukaryota; Metazoa; Nematoda;
Rhabditidae; Peloderinae; Caen
NCBI_TaxID=6239;
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SEQUENCE FROM N.;
MEDLINE=99069613
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Primates;
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19; Mismatches
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No. 2e-37
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Pfam; PF03820; Mtc; 1.
TIGRPAMB; TIGR00798; mtc
SEQUENCE 340 AA; 371;
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Biochem. Biophys
EMBL; AB056724;
SEQUENCE 342 A
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TISSUE=Brain;
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Miyake S., Yama
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Q1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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78. Res. Commun. 295:463-468(2002).
BAC15564.1; -.
AA; 37304 MW; DC2E93A165E95F4B C
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ity 38.3%; Pred. No. 5.8e-36;
servative 50; Mismatches 99; Indels 7;
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shita T., Taniguchi M., Tamatani M., Sato
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the RIKEN Genome Exploration Research G:
"Analysis of the mouse transcriptome bar
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
EMBL; AK036285; BAC29372.1; -.
EMBL; AK082073; BAC38403.1; -.
SEQUENCE 342 AA; 37328 MW; 9BDB8261
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Cerebellum;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
The FANTOM Genome Exploration Researc
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Sideroflexin 5.
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SEQUENCE FROM N.A.

STRAIN=S288C;

Cheret G., Bernardi A., Sor F.J.;

EMBL; X89633; CAA99495.1;

EMBL/GenBank/DDBJ databases.

EMBL; X89633; CAA99495.1;

EMBL; X89633; CAA61777.1;

SGD; S0005797; YOR271C.

InterPro; IPR004686; Mtc.

Pfam; PF03820; Mtc; 1.

TIGRFAMB; TIGR00798; mtc; 1.

Hypothetical protein.

SEQUENCE 327 AA; 35414 MW; FD175626E63B8619 CRC64;
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The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II
"Analysis of the mouse transcriptome based on functional
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
EMBL; AK043706; BAC31624.1; -.
SEQUENCE 302 AA; 32783 MW; 650F6A997043EF26 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
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(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 22, Last annotation update)
V reading frame ORF YOR271C.
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Search completed: February Job time : 44 secs
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RESULT 2 US-09-867-550-1344

Sequence Patent No

NO.

GENERAL INFORMATION: APPLICANT: Leach, N

APPLICANT:

Mehraban,

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Sequence 8, Application US/09990415A; Patent No. US20020165182A1; GENERAL INFORMATION:
APPLICANT: Pharmacia AB
TITLE OF INVENTION: Protein Cluster I
FILE REFERENCE: 00349
CURRENT APPLICATION NUMBER: US/09/990,
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.0
LENGTH: 322
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Law, Debbie
APPLICANT: Topper, James
TITLE OF INVENTION: No. US20020082206A1el Politic Prints of Invention: Thereby
FILE REFERENCE: 21402-013 (Cura-313)
CURRENT APPLICATION NUMBER: US/09/867,550
PRIOR APPLICATION NUMBER: USN 60/208,427
PRIOR APPLICATION NUMBER: USN 60/208,427
NUMBER OF SEQ ID NOS: 2125
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 266
TYPE: PRT
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|PAMAIPPLIMDTLEKKDFLK 261
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Similarity 100.0%;
51; Conservative 0
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Pred. No. 2.2e-141;
Mismatches 0;
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PRIOR FILING DATE:
NUMBER OF SEQ ID NO:
SOFTWARE: Patentin 1
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Publication No. US20030092614A1
GENERAL INFORMATION:
APPLICANT: Herath, et al.
TITLE OF INVENTION: ADPI-41, A NOVEL PROTEIN ISOLATED FROM BRAIN TISSUE HOMOGENATE
FILE OF INVENTION: USES THEREFOR
FULE REFERENCE: 9195-077
CURRENT APPLICATION NUMBER: US/10/014,338
CURRENT FILING DATE: 2002-05-01
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; OTHER INFORMATION: Xaa=A,T,G or
US-09-990-415A-8
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                       1 81.0%; Score 1089; DB 15;
Similarity 78.5%; Pred. No. 1.1e-112;
)1; Conservative 28; Mismatches 27;
                   TEPLIMOTE
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